1 G G A C A G C G T C C A A C C C G G	2 G G A C A G C G T C C G A C C T G G	4 G G A C A G C G T C C G A C T C G	OF SEGROAGE COMPOSES	YPE 7 G G A C A G C G T C C G G C C C G G G C C C G G G C C C G G G C C C G G G C C C G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C G G G G C C C C G G G G C C C C G G G G C C C C G G G G C C C C G G G G C C C C C G G G C C C C C G G G C C C C G G G C C C C C C G G G C C C C C C G G G C C C C C C G G G C C C C C C G G G C C C C C C G G G C C C C C C G G G C	0 A O O O O A P O O O O O O O O	a R 9 G G A C G G C C C C C G A C C F G G	0 106ACGGCGHCCGACCGG	NUMB	PSER 123456789011234567891112345678	PS POST 3102 3409 3438 3603 4054 4082 1199 1239 1248 1265 1482 1499 1509 1552 1593 1616	8 6 7 9 3 4 0 9 3 9 2
11 GGACGGCGTCCGACCTGG	2 199409999909900F99	HA 13 GGACGGCGTCTGACCTGG	OT L1GGACGGFGFCCGGCCFGG	PES PES PES PES PES PES PES PES PES PES	NA COCCAGCGTCCGACCTGG	* 7 ER 16 G G C A G T G T C C G A C C C G G	1 G T A C A A C G T C T G A C C T G G	9 1GTACAGOGTCCCACCTAG	0 26 TACAGCGTCCGGCCTGG	PS ^b NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	PS POSITION° 3102 3409 3438 3603 4054 4082 112359 12359 12485 12485 14990 15099 15099 15593 15593

		на	PLOT	YPE	NUMB:	ERª	PS ^b	PS
21	22	23	24	25	26	27	NUMBER	POSITION
G	G	G	G	G	G	T	1	3102
T	T	Ŧ	T	Ţ	T	G	2	3409
A	Ā	Ä	A	A	G	G	3	3438
C	C	C	С	Ģ	Ċ	C	4	3603
A	A	A	G	A	A	A	5	4054
G	G	G	G	G	G	G	6	4082
ā	c	c	C	Ċ	С	Ċ	7	11998 ·
G	G	G	G	G	G	G	8	12356
T	T	T	T	T	${f T}$	\mathbf{T}	9	12397
C	C	T	Ċ	С	C	C	10	12489
T	T	${f T}$	${f T}$	${f T}$	С	C	11	12653
Ģ	G	G	Ġ	G	G	G	12	14824
A	A	A	A	A	A	A	13	14990
C	C	С	C	C	C	C	14	15089
Ç	C	Ç	Ç	Ċ	C	С	15	15093
С	T	T	T	\mathbf{T}	С	T	16	15529
G	G	G	G	G	Ģ	G	17	15932
G	G	. G	G	G	G	Α	18	16165

^aAlleles for haplotypes are presented 5' to 3' in each column

2. The method of claim 1, wherein the nucleic acid sample contains the second copy of the individual's TNFRSF1A gene to identify [A method for haplotyping the tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene of an individual, which comprises determining which of the TNFRSF1A haplotype pairs shown in the table immediately below defines both copies of the individual's TNFRSF1A gene, wherein the determining step comprises identifying] the phased sequence of nucleotides present at each of PS1-PS18 on the second copy [both copies] of the individual's TNFRSF1A gene,

comparing the phased sequence of the second copy to the TNFRSF1A haplotypes represented in Table 5; and

assigning to the individual, for the second copy of the individual's TNFRSF1A gene, a TNFRSF1A haplotype selected from the TNFRSF1A haplotypes represented in Table 5 which is consistent with the phased sequence of that second copy.[, and wherein each of the TNFRSF1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

^bPS = polymorphic site;

Position of PS within SEQ ID NO:1.]

								m mb	
	IYPE PA							PS ^b	P\$
12/12	22/22	2/2	22/20	12/10	2/1	22/23	2/11	NUMBER	POSITION
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/G	T/T	G/G	T/T	G/G	G/G	T/T	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	3	3438
C/C	C/C	c/c	c/c	c/c	c/c	c/c	c/c	4	3603
G/G	A/A	A/A	A/A	G/G	A/A	A/A	A/G	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
c/¢	Ç/Ç	c/c	c/c	C/C	c/c	C/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	\mathbf{T}/\mathbf{T}	T/T	\mathtt{T}/\mathtt{T}	T/T	\mathbf{T}/\mathbf{T}	T/T	T/T	9	12397
c/c	c/c	c/c	c/c	C/C	c/c	C/T	c/c	10	12489
c/c	T/T	c/c	T/C	C/C	C/C	T/T	c/c	11	12653
G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G	12	14824
G/G	A/A	A/A	A/G	G/A	A/A	A/A	A/A	13	14990
c/c	c/c	C/C	c/c	C/C	c/c	c/c	c/c	14	15089
C/C	C/C	C/C	c/c	c/c	¢/¢	C/C	c/c	15	15093
T/T	T/T	C/C	T/T	T/C	C/C	T/T	C/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
				`					
HAPLO	TYPE PA	IRa						PS ^b	PS
2/19	3/14	12/1	5 22/8	2/9	3/21	2/15	12/17	NUMBER	
G/G	G/G	G/G	G/G	G/G	G/G	G/G	Ģ/Ģ	1	3102
G/T	G/G	G/G	T/G	G/G	G/T	G/G	G/G	2	3409
A/A		_	m. /m.	20 / 20	A/A	2 10	2 / 4	~	
	A/A	A/G	A/A	A/A		A/G	A/G	3	3438
c/c	A/A C/C	A/G C/C	A/A C/C	C/C	c/c	C/C	C/C	4	3603
C/C A/A						C/C A/A	C/C G/A	4 5	3603 4054
	c/c	c/c	c/c	c/c	C/C A/A G/G	C/C A/A G/G	C/C G/A G/G	4 5 6	3603 4054 4082
A/A	C/C A/G	C/C G/A	C/C A/G	C/C A/G	C/C A/A G/G C/C	C/C A/A	C/C G/A G/G C/T	4 5 6 7	3603 4054 4082 11998
A/A G/G	C/C A/G G/G	C/C G/A G/G	C/C A/G G/G	C/C A/G G/G	C/C A/A G/G	C/C A/A G/G	C/C G/A G/G	4 5 6 7 8	3603 4054 4082 11998 12356
A/A G/G C/C	C/C A/G G/G C/T	C/C G/A G/G C/C	C/C A/G G/G C/C	C/C A/G G/G C/C	C/C A/A G/G C/C G/G T/T	C/C A/A G/G C/C G/G T/T	C/C G/A G/G C/T G/G T/T	4 5 6 7 8 9	3603 4054 4082 11998 12356 12397
A/A G/G C/C G/G T/T	C/C A/G G/G C/T G/G	C/C G/A G/G C/C G/G T/T	C/C A/G G/G C/C G/A	C/C A/G G/G C/C G/G	C/C A/A G/G C/C G/G	C/C A/A G/G C/C G/G	C/C G/A G/G C/T G/G T/T C/C	4 5 6 7 8 9	3603 4054 4082 11998 12356 12397 12489
A/A G/G C/C G/G T/T C/C	C/C A/G G/G C/T G/G T/T C/C	C/C G/A G/G C/C G/G T/T C/C	C/C A/G G/G C/C G/A T/T	C/C A/G G/G C/C G/G T/C	C/C A/A G/G C/C G/G T/T	C/C A/A G/G C/C G/G T/T	C/C G/A G/G C/T G/G T/T	4 5 6 7 8 9 10	3603 4054 4082 11998 12356 12397 12489 12653
A/A G/G C/C G/G T/T C/C	C/C A/G G/G C/T G/C C/C	C/C G/A G/G C/C G/G T/T C/C	C/C A/G G/G C/C G/A T/T C/C	C/C A/G G/G C/C G/G T/C C/C	C/C A/A G/G C/C G/G T/T C/C	C/C A/A G/G C/C G/G T/T C/C	C/C G/A G/G C/T G/G T/T C/C	4 5 6 7 8 9 10 11 12	3603 4054 4082 11998 12356 12397 12489 12653 14824
A/A G/G C/C G/G T/T C/C G/G	C/C A/G G/T G/T C/C G/G	C/C G/A G/G C/C G/G T/T C/C C/C	C/C A/G G/G C/C T/T C/C G/G	C/C A/G G/C G/C G/C C/C G/G	C/C A/A G/C G/G T/T C/T G/G	C/C A/A G/G C/C G/T C/C G/G	C/C G/G G/T G/T C/C C/C	4 5 6 7 8 9 10	3603 4054 4082 11998 12356 12397 12489 12653
A/A G/G C/C G/G T/T C/C C/C G/G A/A	C/G G/T G/T C/C G/G A/G	C/C G/A G/G C/C G/G T/T C/C G/G G/A	C/C A/G G/G C/C T/T C/C G/G A/G	C/C A/G G/G C/C G/G T/C C/C	C/C A/A G/C C/C G/T C/T	C/C A/A G/G C/C G/G T/T C/C	C/A G/G G/T G/T C/C G/G	4 5 6 7 8 9 10 11 12 13 14	3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089
A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	C/G G/T G C/C G/C G/C G/C G/C G/C G/C G/C G/C G	C/C G/A G/G C/C G/G T/T C/C G/G G/A C/C	C/C A/G G/G C/C T/T C/C G/G A/G C/C	C/C A/G G/C C/C G/C C/C G/A C/C	C/C A/A G/C G/G T/C C/T C/A	C/C A/A G/G C/C G/G T/T C/C G/G A/A	C/A G/G T/C G/T/C G/A G/A	4 5 6 7 8 9 10 11 12 13	3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093
A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	C/G G T G C G A C C	C/C G/A G/G C/C G/G C/C G/A C/C C/C	C/C A/G G/C A/T C/C G/G A/C C/C	C/C A/G G/C G/C C/C G/A C/C	C/A G/C G/T C/T C/A C/A C/C	C/C A/A G/G C/C G/G T/C C/C G/G A/A C/C	C/A G/FG G/TC G/A C/C G/A C/C	4 5 6 7 8 9 10 11 12 13 14	3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529
A/A G/G C/C G/C C/C C/C G/G A/A C/C C/T	C/G G T G C C G A C C T C C G A C C C T C C G A C C C T C C G A C C C T C T C C T C C T C C T C C T C C T C C T C C T C C T C C T C C T C C T C C T C C T C C C T C C C T C C C T C C C T C C C T C C C T C C C C T C C C C T C C C C C T C C C C C C T C	C/C G/A G/G C/C G/G C/C G/A C/C C/C	C/C A/G G/C T/C C/C T/C C/C T/T	C/C A/G G/C C/C G/C C/C G/A C/C	C/A G/CG T/CT G/A C/C T/CT G/A C/C	C/C A/A G/C G/T C/C G/A C/C	C/AG TG TC CG G/CCG TC CCG GC/CCG TC CCG GC/CCG GC/CCG GC/CCCG GC/CCCG GC/CCCG GC/CCCG GC/CCCG GC/CCCG GC/CCCG GC/CCCG GC/CCCCG GC/CCCG GC/CCCCG GC/CCCCG GC/CCCCG GC/CCCCG GC/CCCCG GC/CCCCG GC/CCCCG GC/CCCCCCG GC/CCCCCCCG GC/CCCCCCCC	4 5 6 7 8 9 10 11 12 13 14 15	3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529 15932
A/A G/G C/C G/G T/T C/C C/C G/G A/A C/C	C/G G T G C G A C C	C/C G/A G/G C/C G/G C/C G/A C/C C/C	C/C A/G G/C A/T C/C G/G A/C C/C	C/G A/G G/C G/C G/C G/A C/C G/T	CAGCGTCTGACCCT/	C/C A/A G/G C/C G/T C/C G/A C/C C/C	C/AG TG TC CG G/CCG TC CGG TC CCG TC CCG TC CCG TC CCG TC CCG TC CCT TC TC	4 5 6 7 8 9 10 11 12 13 14 15 16	3603 4054 4082 11998 12356 12397 12489 12653 14824 14990 15089 15093 15529

						· ·			
HAPLOT	YPE PAI	[Rª						₽ S ^b	PS
2/21	22/3	22/25	12/25	12/24	12/13	3/16	22/16	NUMBER	POSITION
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	1	3102
G/T	T/G	T/T	G/T	G/T	G/G	G/G	T/G	2	3409
A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/G	3	3438
c/c	C/C	C/G	C/G	C/C	C/C	C/C	C/C	4	3603
A/A	A/A	A/A	G/A	G/G	G/G	A/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	6	4082
c/c	¢/c	d/d	C/C	¢/c	c/c	C/C	c/c	7	11998
G/G	G/G	G/Ġ	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
c/c	c/c	c/c	c/c	c/c	C/C	c/c	C/C	10	12489
C/T	T/C	T/T	C/T	C/T	C/T	C/C	T/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/A	A/A	A/A	G/A	G/A	G/A	A/A	A/A	13 .	14990
c/c	c/c	C/C	c/c	C/C	c/c	C/C	c/c	14	15089
c/c	C/C	C/C	C/C	c/c	c/c	C/C	c/c	15	15093
C/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	18	16165
*** *** ***		- m A						PSb	PS
	YPE PA	TK	0.406	22/11	12/7	22/2	22/18	ro NUMBER	POSITION°
3/27	22/10	2/16	2/26	G/G	G/G	44/4 G/G	G/G	1	3102
G/T	G/G	G/G	G/G		G/G	T/G	T/T	2	3409
G/G	T/G	G/G	G/T	T/G A/A	A/A	A/A	A/A	3	3438
A/G	A/A C/C	A/G C/C	A/G C/C	C/C	C/C	c/c	C/C	4	3603
C/C			A/A	A/G	G/A	A/A	A/A	5	4054
A/A	A/G	A/A	G/G	G/G	G/G	G/G	G/A	6	4082
G/G	G/G	G/G C/C	c/c	C/C	C/C	c/c	C/C	7	11998
C/C	C/C G/G	G/G	G/G	G/G	G/G	G/G	G/G	8	12356
G/G T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	9	12397
	C/C	C/C	C/C	c/c	C/C	c/c	d/d	10	12489
C/C		c/c	d/d	T/C	c/c	T/C	T/T	11	12653
C/C	T/C G/G	G/G	G/G	G/G	G/G	G/G	G/G	12	14824
G/G	A/A		A/A	A/A	G/G	A/A	A/A	13	14990
A/A		A/A	C/C	C/C	C/C	Ç/Ç	c/c	14	15089
C/C	C/C	C/C	G/G	C/G	c/c	c/c	c/c	15	15093
C/C	C/C	C/C	C/C	17/I	で/で	T/C	T/T	16	15529
T/T	T/C	C/T							
G/G G/A	G/G G/G	G/G G/G	G/G G/G	G/G G/G	G/G G/G	G/G G/G	G/G G/G	17 18	15932 16165

HAPLOT	CYPE PA	.I.Rª				PSb	PS
22/12	12/5	12/3	12/2	14/6	16/4	NUMBER	POSITIONS
G/G	G/G	G/G	G/G	G/G	G/G	1	3102
T/G	G/G	G/G	G/G	G/G	G/G	2	3409
A/A	A/A	A/A	A/A	A/A	G/A	3	3438
C/C	c/c	c/c	c/c	c/c	c/c	4	3603
A/G	G/A	G/A	G/A	G/A	A/A	5	4054
G/G	G/G	G/G	G/G	G/Ģ	G/G	6	4082
C/C	c/c	c/c	c/c	T/C	C/C	7	11998
G/G	G/G	G/G	G/G	G/G	G/G	8	12356
T/T	T/T	T/T	T/T	T/T	T/T	9	12397
c/c	.c/c	C/C	c/c	C/C	C/C	10	12489
T/C	C/C	C/C	C/C	C/C	C/C	11	12653
G/G	G/G	G/G	G/G	G/G	G/G	12	14824
A/G	G/A	G/A	G/A	G/G	A/A	13	14990
C/C	C/T	c/c	C/C	c/c	c/c	14	15089
C/Ç	C/C	c/c	C/C	C/C	C/T	15	15093
T/T	T/C	T/T	T/C	T/C	T/C	16	15529
G/G	G/G	G/G	G/G	G/G	G/G	17	15932
G/G	G/G	G/G	G/G	G/G	G/G	18	16165

^aHaplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5' to 3' as 1st polymorphism/2nd polymorphism in each column; ^bPS = polymorphic site;

An isolated polymoleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a first nucleotide sequence which comprises a tumor necrosis factor receptor superfamily, member 1A

(TNFRSF1A) isogene encoding a TNFRSF1A polypeptide with a domain capable of binding TNFa, wherein the TNFRSF1A isogene comprises nucleotides 2920-4210, 11417-12926, and 14634-16768 of SEQ ID NO:1 except the sequence is substituted by the combination of nucleotides at polymorphic sites 1 to 18 (PS1-PS18) defined by a TNFRSF1A haplotype [is] selected from the group consisting of TNFRSF1A haplotypes

[isogenes] 1-27 shown in Table 5, wherein the nucleotide positions of PS1-PS18 in SEQ ID NO:1 and the alleles at each of PS1-PS18 for each TNFRSF1A haplotype in the group are set forth in Table 5; and the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-27 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

Position of PS in SEQ ID NO:1.]

	2 G G A C A G C G T C C G A C C C	E 4 G G A C A G C G T C C G A C T C G	N 5 G G A C A G C G T C C G A T C C G	TOGACAGOGTOCGGCCCGG	@@@C@@O@#OC@@OO#	9664066060000040046	0	PS ^b NUMB: 1 2 3 4 5 6 7 8 9 10 1 2 3 1 1 1 1 5 6 7 1 1 2 3 1 1 5 6 7 1 1 2 3 1 1 5 6 7 8 9 1 1 1 2 3 1 1 5 6 7 8 9 1 1 1 2 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ER	PS POSITION° 3102 3409 3409 34054 4052 11998 123597 124653 14999 126524 15089 15529 15932	SEQ ID NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EX. 2922922922922921144114461144611446114461	310N MMINED ⁴ 20-4210 20-4210 20-4210 20-4210 20-4210 217-129 117-129 117-129 117-129 117-129 117-129 117-129 117-129 117-129 117-129 117-129	26 26 26 26 26 26 88 68 68	
G		G G	G	GG	_	G	G	18		16165	1		534-167		
		E S C A C G G C G F C F G A C C F G G	NUMBER OF A COUNTY	R 1 G G G C A G C G T C C G A C C C G G	6 166604606H006400H66	10 G G C A G H G F C C G A C C C G G	80 1 4 0 4 4 0 6 4 0 6 4 6 6 6 6 6 6 6 6 6 6	19 19 19 19 19 19 19 19 19 19 19 19 19 1	0 26FACAGCGFCCGGCCFGG	PS ^b NUMBER 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	PS POSITIO 3102 3409 3438 36054 4052 119956 123485 146524 149989 150523 155936 1616	SEC 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO. 2920-4 2920-4 2920-4 2920-4 2920-4 11417- 11417- 114634- 14634- 14634- 14634- 14634- 14634- 14634- 14634-	210 210 210 210 210 2210 -12926 -12926 -12926 -16768 -16768 -16768 -16768 -16768	

3:44PM



	ISOG	ENE	NUMB	ERª		PS ¹	3	PS	SEQ ID	REGION
21	22	23	24	25	26	27	NUMBER	POSITION	a NO.	EXAMINED
G	G	G	G	G	G	T	1	3102	1	2920-4210
\mathbf{T}	${f T}$	\mathbf{T}	Ŧ	T	Т	Ģ	2	3409	1	2920-4210
A	A	A	A	A	G	G	3	3438	1	2920-4210
C	С	C	С	G	C	C	4	3603	1,	2920-4210
A	A	A	G	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	6	4082	1	2920-4210
C	C	Ç	Ç	¢	C	C	7	11998	1	11417-12926
G	G	G	G	G	G	G	8	12356	1	11417-12926
T	卫.	T	\mathbf{T}	T	Ŧ	Ţ	9	12397	1	11417-12926
C	C	\mathbf{T}	Ç	C	Ç	¢	10	12489	1.	11417-12926
T	T	T	T	T	C	С	11	12653	1	11417-12926
G	Ģ	G	Ġ	Ģ	G	G	12	14824	1	14634-16768
A	A	A	A	A	A	A	13	14990	1 ,	14634-16768
C	C	C	C	C	C	C	14	15089	1	14634-16768
C	¢	¢	Ç	C	C	C	15	15093	1	14634-16768
С	T	T	${f T}$	·T	С	T	16	15529	1	14634-16768
G	G	G	G	G	Ģ	G	17	15932	1	14634-16768
G	G	G	G	G	Ģ	A	1.8	1,6165	1	14634-16768

^{*}Alleles for isogenes are presented 5' to 3' in each column;

(b) a second nucleotide sequence which is complementary to the first nucleotide sequence.

24. An isolated fragment of a tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A) isogene, wherein the fragment comprises at least 15 [10] nucleotides in one of the regions of SEQ ID NO:1 selected from nucleotides 2920-4210, 11417-12926, or 14634-16768 [shown in the table immediately below] and wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at PS1, guanine at PS4, adenine at PS12, thymine at PS14, thymine at PS15, adenine at PS17 and adenine at PS18, wherein the nucleotide positions in SEO ID NO:1 of the [selected] polymorphisms are 3102 for PS1. 3603 for PS4, 14824 for PS12, 15089 for PS14, 15093 for PS15, 15932 for PS17 and 16165 for PS18. [has the position set forth in the table immediately below:

^bPS = polymorphic site;

Position of PS in SEQ ID NO:1;

⁴Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.]



		I	sog	ENE	NŲ	MBI	CR ^a			PS ¹	þ	PS	SEQ ID			
1	2	3	4	5	6	7	8	9	10	NUMBI	ΞR	POSITION ²	NO.		MINE	
G	G	G	G	G	G	G	G	G	G	1		3102	1		0-42	
G	Ģ	G	G	Ģ	G	G	G	G	G-	2		3409	1		0-42	
A	A	A	A	A	A	A	A	A	A	3		3438	1		0-42	•
ď	ď	C	C	C	Ċ	¢	Ç	C	С	4		3603	1	292	0-42	10
æ.	Ā	A	Ā	Ā	Ā	Α	Ġ	G .	Ġ	5		4054	1	292	0-42	10
G	G	G	G	G	G	G	G	G	G	. 6		4082	1	292	0-42	10
Ç	č	Ĉ	ā	ç	ā	Ċ	ā	Ċ	C	7		11998	1	114	17-1	2926
Ğ	G	G	Ġ	Ğ	Ģ	Ģ	Ā	G	G	8		12356	1	114	17-1	2926
Ţ	Ţ	Ī	T	Ī	T	Ţ	T	Ç	Ť	9		12397	1	114	17-1	2926
ē	ć	ā	ō	ā	Ĉ	ā	Ċ	Ċ	Ç	10		12489	1	114	17-1	2926
ā	ā	ē	Ċ	Ğ.	¢	Ċ	Ċ	Ċ	Ċ	11		12653	1	114	17-1	2926
Ā	Ğ	G	G	Ğ	Ğ	G	G	G	G	12		14824	1	146	34-1	6768
A	Ā	Ā	Ā	Ā	G	Ģ	Ğ	A	A	13		14990	1	146	34-1	6768
Ç	Ç	Ċ	Ĉ	T	č	č	Č	ā	¢	14		15089	i	146	34-1	6768
Č	Č	Č	T	Ĉ	č	Ç	Ç	č	č	15		15093	1	146	34-1	6768
Č	c	Ť	ċ	Ċ	Č	T	Ī	T	Č	16		15529	ī			6768
G	G	Ĝ	Ğ	G	G	Ġ	Ġ	Ğ	Ğ	17		15932	1			6768
G	G	G	Ğ	G	G	Ğ	Ğ	Ğ	G	18		16165	ī	1.46	34-1	6768
	•	Φ	ų.	Ų	•==	4	·	·	-				_			
			ISOG			MB:						₽Sp	PS	SEQ		REGION
11	1:	2	13	14	1	5	16	17	18	19	20	NUMBER	POSITI		NO.	EXAMINED
G	G		G	G	G		Ģ	G	G	G	G	1	3102	1		920-4210
G	G		G	G	G	ł	G	G	T	T	Ţ	2	3409	1		920-4210
A	A		A	A	Ġ	÷	Ģ	G	A	A	Α	3	3438	1		920-4210
¢	C		C	С	C	!	C	C	Ç	Ç	Ç	4	3603	1		920-4210
G	G		G	G	.A		A	A	A	A	A	5	4054	1		920-4210
Ġ	Ġ		Ģ	G	G	ł	G	G	A	G	G	6	4082	1		920-4210
C	C		C	T	C	;	C	T	Ċ	Ç	C	7	11998	1		1417-12926
G	G		Ģ	G	Ģ	ļ	Ģ	G	G	G	Ģ	8	12356	1		1417-12926
T	\mathbf{T}		T	T	Т	•	\mathbf{T}	Ţ	\mathbf{T}	\mathbf{T}	T	9	12397	1		1417-12926
Ç	Ç		С	С	C	:	C	C.	С	С	C	10	12489	1		.1417-12926
C	C		T	C	C	:	Ç	¢	${f T}$	C	C	11	12653	1,		.1417-12926
G	G		Ģ	Ġ	G	}	G	· G	G	Ģ	G	12	14824	1	1	4634-16768
A	G		A	G			A	A	A	A	G	13	14990	1	1	4634-16768
Ç	ç		C	Ĉ	Ċ		Ĉ	C	Ç	¢	C	14	15089	1	1	4634-16768
Ğ,	ā		C	C	C	:	Ċ	C	C	C	Ç	15	15093	1	1	.4634-16768
T	Ţ		Ţ	Ť	č		T	C	T	T	Ť	16	15529	1		4634-16768
Ğ	Ĝ		Ğ	G	G		G	G	G	A	Ģ	17	15932	1	1	.4634-16768
Ģ	G		Ğ	Ğ	G		Ğ	G	G	G	G	18	16165	1	1	4634-16768

		ISOG	ENE	NUME	BER		PS ^b	PS	SEQ ID	REGION
21	22	23	24	25	26	27	NUMBER	POSITION ^e	NO.	EXAMINED ^d
G	G	G	G	Ģ	G	T	1	3102	1	2920-4210
T	T	${f T}$	\mathbf{T}	T	T	G	2	3409	1	2920-4210
A	A	A	A	A	G	G	3	3438	1	2920-4210
C .	С	С	Ç	G	¢	С	4	3603	1	2920-4210
A	A	A.	G	A	A	A	5	4054	1	2920-4210
G	G	G	G	G	G	G	6	4082	1	2920-4210
C	Ç	¢	Ċ	C	C	C	7	11998	1	11417-12926
G	G	G	G	G ·	G	G	8	12356	1	11417-12926
\mathbf{T}	Т	T	Ŧ	T	\mathbf{T}	\mathbf{T}	9	12397	1	11417-12926
Ç '	С	T	C	C	C	C	10	12489	1	11417-12926
T	\mathbf{T}	\mathbf{T}	${f T}$	T	C	¢	11	12653	1	11417-12926
Ġ	G	G	G	G	G	G	12	14824	1	14634-16768
A	A	A	A	A	A	A	13	14990	1	14634-16768
¢	C	C	C	С	C	C	14	15089	1,	14634-16768
C	C	С	C	Ç	¢	C	15	15093	1	14634-16768
Ç	T	Т	Т	Ψ	Ċ	T	16	15529	1	14634-16768
G	G	G	G	G	G	G	17	15932	1	14634-16768
G	Ģ	G	G	G	Ģ	A	18	16165	1	14634-16768

Alleles for isogenes are presented 5' to 3' in each column;

25. An isolated polynucleotide comprising a TNFRSF1A coding sequence, [wherein the coding sequence is selected from the group consisting of 8, 9, 14, 17, and 19 shown in the table immediately below, and] wherein [each of] the coding sequence comprises SEQ ID NO:2, except for being substituted with an adenine at position 935. [at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

Isog	ene	Coding	Sequence	Number	PS	PS
₽ _	9	14,17	19		Number	Position
a	C	T	С		7	224
A	G	G	G		8	362
T	C	T	T		9	403
G	G	G	A		17	935

^aAlleles for the isogene coding sequence are presented 5' to 3' in each column; the numerical portion of the isogene coding sequence number represents the number of the parent full TNFRSF1A isogene; ^bPS = polymorphic site;

Please cancel claim 33.

Please add the following new claims:

^bPS = polymorphic site;

[&]quot;Position of PS in SEQ ID NO:1;

^dRegion examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the sequenced region.]

Position of PS in SEQ ID NO:2.]

- 35. The isolated polynucleotide of claim 20, wherein the isogene encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 and wherein the isogene is selected from the group consisting of isogenes 1,2,3,4,5,6,7,10,11,12,13,15,16,18,20, 21,22, 23,24,25,26 and 27.
- 36. The isolated polynucleotide of claim 20, wherein the isogene is isogene 19, encoding a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a lysine at amino acid position 312.
- 37. The isolated polynucleotide of claim 20, wherein the isogene is isogene 8 and encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a glutamine at amino acid position 121.
- 38. The isolated polynucleotide of claim 20, wherein the isogene 9 and encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a histidine at amino acid position 135.
- 39. The isolated polynucleotide of claim 20, wherein the isogene is selected from isogenes 14 and 17 and encodes a TNFRSF1A polypeptide identical to SEQ ID NO:3 except for having a leucine at amino acid position 75.

A clean version of the amended claims is attached hereto.

